

National Security Pathogen Sequencing Project

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For

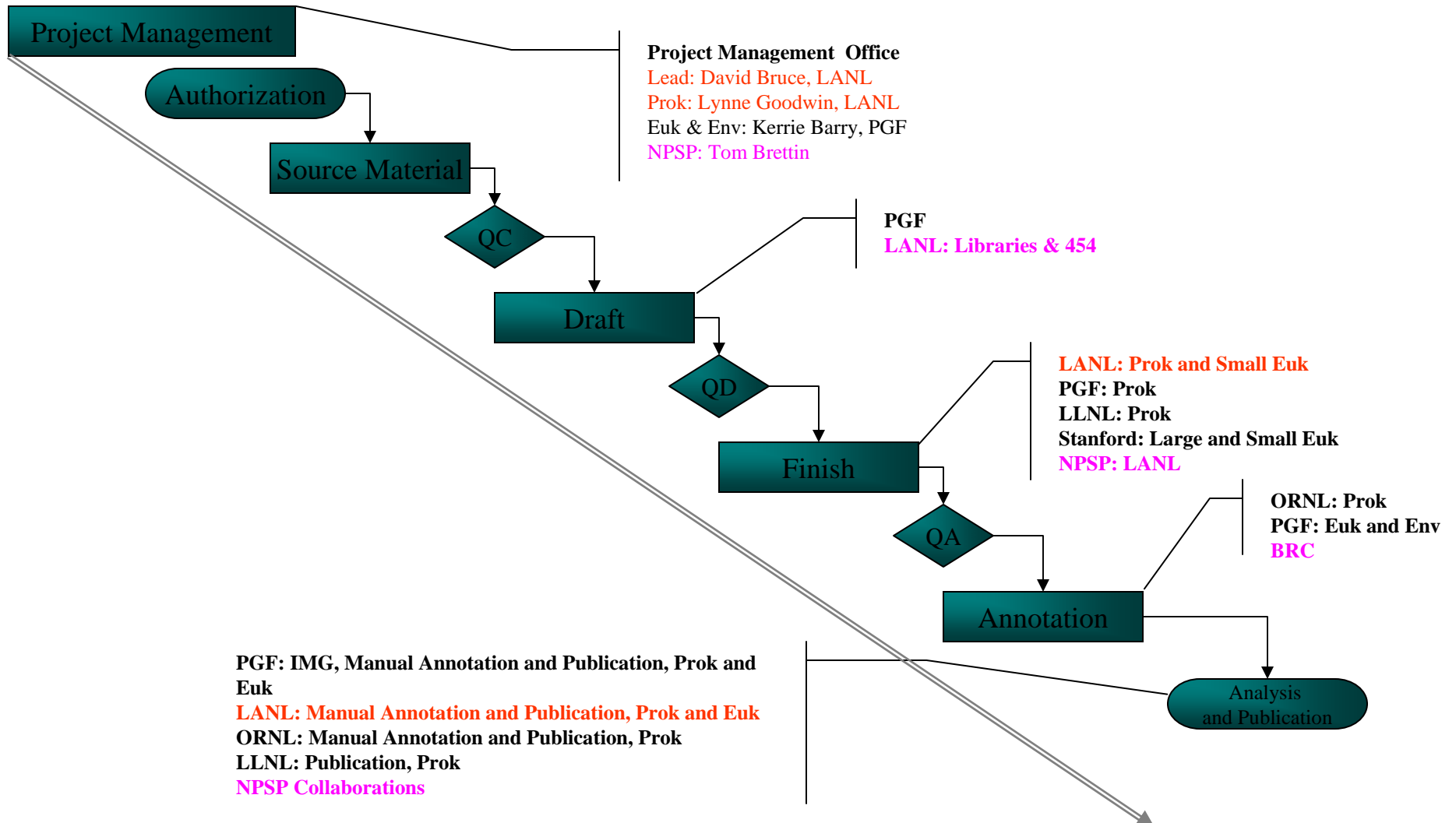
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National Security Pathogen Sequencing Project



DOE Joint Genome Institute

- **JGI Members**
 - Production Genomics Facility, Walnut Creek CA (JGI-PGF)
 - Los Alamos National Laboratory (JGI-LANL)
 - Lawrence Livermore National Laboratory (JGI-LLNL)
 - Oak Ridge National Laboratory (JGI-ORNL)
 - Stanford University (JGI-Stanford)
- **JGI-LANL specializes in finishing and manual annotation**
- **National Security Pathogen Sequencing Project utilizes “Work for Others” mechanism at JGI**

Microbial Sequencing at the JGI: DOE JGI-LANL LANL National Pathogen Sequencing Project



Changes in the last year

- **Paul Gilna resigned as JGI-LANL Center Director and became UCSD CAMERA Executive Director**
- **Major deliverable shift: Draft quality to finish quality**
- **Draft strategy shift to 5X Sanger, ~ 5X 454**
- **Karen Hill (LANL) joined team as phylogenetic consultant to sponsor**
 - **Particularly *C. botulinum*, *B. anthracis*, *Y. pestis***
- **Current performance period ends this fiscal year**



JGI-LANL Finished Microbes

National Security Pathogen Sequencing Project

| Finish Date | Non-Pathogen | Pathogen | Total |
|-----------------------------|--------------|-----------|------------|
| December-04 | 2 | | 2 |
| January-05 | 1 | | 1 |
| April-05 | 3 | | 3 |
| May-05 | 3 | | 3 |
| July-05 | 1 | | 1 |
| August-05 | 1 | | 1 |
| September-05 | 3 | | 3 |
| October-05 | 3 | | 3 |
| November-05 | 2 | 1 | 3 |
| December-05 | 2 | | 2 |
| January-06 | 3 | | 3 |
| February-06 | 1 | 1 | 2 |
| March-06 | 4 | | 4 |
| April-06 | 8 | | 8 |
| May-06 | 5 | 1 | 6 |
| June-06 | 0 | 1 | 1 |
| July-06 | 3 | 1 | 4 |
| August-06 | 5 | | 5 |
| September-06 | 3 | 2 | 5 |
| October-06 | 6 | 2 | 8 |
| November-06 | 4 | 3 | 7 |
| Total Finished | 63 | 12 | 75 |
| In Finishing Process | 46 | 8 | 54 |
| Total Projects | 109 | 20 | 129 |

Current Interactions with BRCs

NIAID BRC Supported Annotation Projects

| Code | Organism | Annotation | Contact | Start Date | Status |
|------------|----------------------------------|------------------|----------------------------|-----------------|------------------|
| CLI | Clostridium botulinum | NIAID BRC | Owen White | 12/28/05 | cancelled |
| BUA | Burkholderia pseudomallei | NIAID BRC | Owen White | 06/13/06 | ongoing |
| YPE | Yersinia pestis | NIAID BRC | Guy Plunkett | 06/13/06 | ongoing |
| FTW | Francicella tularensis | NIAID BRC | Richard Scheuermann | 06/07/06 | ongoing |

NON-NIAID BRC Supported Annotation Projects

| Code | Organism | Annotation | Contact | Start Date | Status |
|------------|------------------------------------|--------------------|-----------------------------------|-----------------|----------------|
| YPT | Yersinia psuedotuberculosis | TIGR | Jacques Ravel | 09/29/06 | ongoing |
| FTA | Francicella tularensis | TIGR | Jacques Ravel | 06/30/06 | ongoing |
| FTM | Francicella tularensis | Western RCE | Paul Keim/Anders Johansson | 12/20/06 | |

Activities this FY

- **Vibrio**
 - Fifteen draft this FY
 - Twenty four more available
- **Rickettsia**
 - Ten to twenty draft this FY
- **Clostridium botulinum**
 - Fifteen draft this FY
- **Actual draft count gDNA supply chain limited**
 - 4 draft / month capacity = ~ 40 slots left this FY
- **Finishing will continue into next FY**
- **BRC potential about 2 finished projects / month for next 6 months – supply chain limited thereafter...**

Collaborations

- Ongoing work with BRC
- Partner with JGI Integrated Microbial Genomics (IMG) group to expedite listing in IMG
 - <http://img.jgi.doe.gov/>
 - Utilize IMG front end QC system for validating annotation
 - Load annotation in IMG concurrent with GenBank submission
- Publications with pathogen suppliers

The screenshot shows the JGI Integrated Microbial Genomes (IMG) website. At the top, there is a JGI logo and a search bar. Below the logo, the text "img" is prominently displayed, followed by "INTEGRATED MICROBIAL GENOMES". A navigation bar includes links for "IMG Home", "Find Genes", "Find Genomes", "Find Functions", "Compare Genomes", "MyIMG", "Analysis Carts", "About IMG", "Using IMG", and "News".

On the left side, there is a table titled "IMG Genomes" showing the status of genome sequencing across different domains:

| finished/draft | JGI | Total |
|----------------|-------|----------|
| Bacteria | 79/24 | 359/238 |
| Archaea | 9/4 | 28/4 |
| Eukarya | 0/0 | 13/0 |
| Viruses | 0/0 | 1661/0 |
| All Genomes | 79/28 | 2059/243 |
| Grand Total | 177 | 2301 |

Below the table, there is a version notice: "Version 2.0 December 1, 2006" and links for "IMG Questions/Comments", "VISTA Questions/Comments", and a "Disclaimer".

The main content area on the right contains several paragraphs of text. The first paragraph describes the IMG system as a framework for comparative analysis of genomes. The second paragraph mentions that the content of IMG 2.0 has been refreshed with the latest versions of all microbial genomes available in RefSeq version 19. The third paragraph describes the IMG user interface, which allows navigating the microbial genome data space. The fourth paragraph explains that microbial genome data analysis in IMG usually starts with the definition of an analysis context. The fifth paragraph provides information on how to use the IMG system, including links to "About IMG" and "Using IMG". The sixth paragraph mentions that users may upload or type in their MyIMG gene annotations. The seventh paragraph states that IMG serves as the foundation for the metagenome data management and analysis system, "IMG/M". The final paragraph indicates the next IMG release date: "Next IMG release: March 1, 2007".

Acknowledgements

- **JGI LANL**
 - Tom Brettin
 - David Bruce
 - Chris Detter
 - Cliff Han
 - Karen Hill
 - Yvonne Rogers
 - Lance Green
 - Christine Munk
- **JGI PGF**
 - Susan Lucas
 - Hope Tice
- **External Collab**
 - Many...